

Output tables for 1xN statistical comparisons.

December 17, 2022

1 Average rankings of Friedman Alligned test

Average ranks obtained by each method in the Friedman Alligned test.

Algorithm	Ranking
MEABC	160.2414
ABCAD	99.069
ABCNG	136.0345
SHADE	66.069
MAPSO	101.5517
TAPSO	92.1379
MEEABC	58.8966

Table 1: Average Rankings of the algorithms (Aligned Friedman)

Aligned Friedman statistic (distributed according to chi-square with 6 degrees of freedom): 24.210573.  
P-value computed by Aligned Friedman Test: 0.000477667116.

## 2 Post hoc comparison (Friedman Alligned)

P-values obtained in by applying post hoc methods over the results of Friedman Alligned procedure.

$i$	algorithm	$z = (R_0 - R_i)/SE$	$p$	Holm	Hochberg	Hommel	Holland	Rom
6	ME/ABC	6.569209	0		0.008333		0.008512	0.008764
5	ABCNG	5.000109	0.000001		0.01		0.010206	0.010515
4	MAPSO	2.764924	0.005694		0.0125		0.012741	0.013109
3	ABCADE	2.603991	0.009215		0.016667		0.016952	0.016667
2	TAPSO	2.154719	0.031184		0.025		0.025321	0.025
1	SHADE	0.464919	0.64199		0.05		0.05	0.05

Table 2: Post Hoc comparison Table for  $\alpha = 0.05$  (FRIEDMAN ALLIGNED)

Bonferromi-Dunn's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.008333$ .  
Holm's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.025$ .  
Hochberg's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.016667$ .  
Hommel's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.025$ .  
Holland's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.025321$ .  
Rom's procedure rejects those hypotheses that have an unadjusted p-value  $\leq 0.016667$ .

### 3 Adjusted P-Values (Friedman Alligned)

Adjusted P-values obtained through the application of the post hoc methods (Friedman Alligned).

i	algorithm	unadjusted $p$	$p_{Bonf}$	$p_{Holtm}$	$p_{Hochberg}$	$p_{Hommel}$
1	MEABC	0	0	0	0	0
2	ABCNG	0.00001	0.000003	0.000003	0.000003	0.000003
3	MAPSO	0.005694	0.034162	0.022774	0.022774	0.018429
4	ABCADE	0.009215	0.055287	0.027644	0.027644	0.027644
5	TAPSO	0.031184	0.187103	0.062368	0.062368	0.062368
6	SHADE	0.64199	3.851939	0.64199	0.64199	0.64199

Table 3: Adjusted  $p$ -values (ALIGNED FRIEDMAN) (I)

i	algorithm	unadjusted $p$	$p_{Holland}$	$p_{Rom}$
1	MEABC	0	0	0
2	ABCNG	0.000001	0.000003	0.000003
3	MAPSO	0.005694	0.022581	0.021716
4	ABCADE	0.009215	0.02739	0.027644
5	TAPSO	0.031184	0.061395	0.062368
6	SHADE	0.64199	0.64199	0.64199

Table 4: Adjusted  $p$ -values (ALIGNED FRIEDMAN) (II)